S. Unger
1642
13

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│ **This Raw Listing contains the General** │
│ **Information Section and up to the first 5 pages.** │
└───┘

```
 1                              SEQUENCE LISTING          ENTERED
 2
 3   (1)      General Information
 4
 5            (i) APPLICANT: Burkly, Linda C.
 6
 7            (ii) TITLE OF THE INVENTION: TREATMENT FOR INSULIN DEPENDENT
 8                     DIABETES
 9
10            (iii) NUMBER OF SEQUENCES: 16
11
12            (iv) CORRESPONDENCE ADDRESS:
13               (A) ADDRESSEE: Fish & Richardson P.C.
14               (B) STREET: 225 Franklin Street
15               (C) CITY: Boston
16               (D) STATE: MA
17               (E) COUNTRY: USA
18               (F) ZIP: 02110-2804
19
20            (v) COMPUTER READABLE FORM:
21               (A) MEDIUM TYPE: Diskette
22               (B) COMPUTER: IBM Compatible
23               (C) OPERATING SYSTEM: DOS
24               (D) SOFTWARE: FastSEQ for Windows Version 2.0
25
26            (vi) CURRENT APPLICATION DATA:
27               (A) APPLICATION NUMBER: 09/234,290
28               (B) FILING DATE: 20-JAN-1999
29
30            (vii) PRIOR APPLICATION DATA:
31               (A) APPLICATION NUMBER: 08/447,118
32               (B) FILING DATE: 22-MAY-1995
33
34               (A) APPLICATION NUMBER: PCT/US94/01456
35               (B) FILING DATE: 09-FEB-1994
36
37               (A) APPLICATION NUMBER: 08/029,330
38               (B) FILING DATE: 09-FEB-1993
39
40            (viii) ATTORNEY/AGENT INFORMATION:
41               (A) NAME: Myers, Louis
42               (B) REGISTRATION NUMBER: 35,965
43               (C) REFERENCE/DOCKET NUMBER: 10274/008003
44
45            (ix) TELECOMMUNICATION INFORMATION:
46               (A) TELEPHONE: 617/542-5070
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47              (B) TELEFAX: 617/542-8906
48
49
50          (2) INFORMATION FOR SEQ ID NO:1:
51
52      (i) SEQUENCE CHARACTERISTICS:
53          (A) LENGTH: 360 base pairs
54          (B) TYPE: nucleic acid
55          (C) STRANDEDNESS: single
56          (D) TOPOLOGY: linear
57
58      (ix) FEATURE:
59          (A) NAME/KEY: Coding Sequence
60          (B) LOCATION: 1...360
61
62      (ix) FEATURE:
63          (A) NAME/KEY: misc_feature
64          (B) LOCATION: 1
65          (D) OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy
66              chain variable region; amino acid 1 is Glu (E) but
67              Gln (Q) may be substituted"
68
69      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
70
71  GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA        48
72  Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
73   1           5                   10                  15
74
75  GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT        96
76  Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
77              20                  25                  30
78
79  ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA       144
80  Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
81          35                  40                  45
82
83  AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG       192
84  Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
85      50                  55                  60
86
87  GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG       240
88  Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
89   65                  70                  75                  80
90
91  CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA       288
92  Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
93              85                  90                  95
94
95  GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA       336
96  Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
97              100                 105                 110
98
99  GGG ACC ACG GTC ACC GTC TCC TCA                                       360·
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100   Gly Thr Thr Val Thr Val Ser Ser
101       115                 120
102
103          (2) INFORMATION FOR SEQ ID NO:2:
104
105       (i) SEQUENCE CHARACTERISTICS:
106          (A) LENGTH: 120 amino acids
107          (B) TYPE: amino acid
108          (D) TOPOLOGY: linear
109
110      (ii) MOLECULE TYPE: protein
111
112       (v) FRAGMENT TYPE: internal
113
114      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
115
116   Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
117    1               5                  10                  15
118   Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
119           20                  25                  30
120   Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
121           35                  40                  45
122   Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
123       50                  55                  60
124   Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
125    65                  70                  75                  80
126   Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
127               85                  90                  95
128   Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
129           100                 105                 110
130   Gly Thr Thr Val Thr Val Ser Ser
131       115                 120
132
133          (2) INFORMATION FOR SEQ ID NO:3:
134
135       (i) SEQUENCE CHARACTERISTICS:
136          (A) LENGTH: 318 base pairs
137          (B) TYPE: nucleic acid
138          (C) STRANDEDNESS: single
139          (D) TOPOLOGY: linear
140
141      (ii) MOLECULE TYPE: cDNA
142
143      (ix) FEATURE:
144          (A) NAME/KEY: Coding Sequence
145          (B) LOCATION: 1...318
146          (D) OTHER INFORMATION:/product= "HP1/2 light chain
147              variable region"
148
149      (ix) FEATURE:
150          (A) NAME/KEY: misc_feature
151          (B) LOCATION: 1
152          (D) OTHER INFORMATION:/note= "pBAG172 insert: HP1/2
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/234,290*

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```
153                       light chain variable region"
154
155          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
156
157   AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA      48
158   Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
159    1               5                  10                  15
160
161   GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT      96
162   Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
163                20                  25                  30
164
165   GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA     144
166   Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
167            35                  40                  45
168
169   TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC     192
170   Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
171         50                  55                  60
172
173   AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT     240
174   Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
175    65                  70                  75                  80
176
177   GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC     288
178   Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
179                85                  90                  95
180
181   ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC                            318
182   Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
183            100                 105
184
185          (2) INFORMATION FOR SEQ ID NO:4:
186
187          (i) SEQUENCE CHARACTERISTICS:
188             (A) LENGTH: 106 amino acids
189             (B) TYPE: amino acid
190             (D) TOPOLOGY: linear
191
192          (ii) MOLECULE TYPE: protein
193
194          (v) FRAGMENT TYPE: internal
195
196          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
197
198   Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
199    1               5                  10                  15
200   Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
201                20                  25                  30
202   Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
203            35                  40                  45
204   Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
205         50                  55                  60
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206    Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
207     65                70                75                80
208    Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
209                     85                90                95
210    Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
211                100               105
212
213          (2) INFORMATION FOR SEQ ID NO:5:
214
215          (i) SEQUENCE CHARACTERISTICS:
216            (A) LENGTH: 429 base pairs
217            (B) TYPE: nucleic acid
218            (C) STRANDEDNESS: single
219            (D) TOPOLOGY: linear
220
221          (ii) MOLECULE TYPE: cDNA
222
223          (ix) FEATURE:
224            (A) NAME/KEY: Coding Sequence
225            (B) LOCATION: 1...429
226
227          (ix) FEATURE:
228            (A) NAME/KEY: sig_peptide
229            (B) LOCATION: 1...57
230
231          (ix) FEATURE:
232            (A) NAME/KEY: mat_peptide
233            (B) LOCATION: 58...429
234
235          (ix) FEATURE:
236            (A) NAME/KEY: misc_feature
237            (B) LOCATION: 1
238            (D) OTHER INFORMATION:/note= "pBAG195 insert: AS heavy
239                  chain variable region"
240
241          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
242
243    ATG GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCA CCA GGT        48
244    Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
245    -19             -15               -10                -5
246
247    GCC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA        96
248    Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
249                 1               5                 10
250
25
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/234,290*

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Line	Error	Original Text